

GenCore version 5.1.3
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OK protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 11:31:04 ; Search time 77 Seconds
(without alignments)
3004.079 Million cell updates/sec

Title: US-09-765-034-2
1747
Perfect score: 1747
Sequence: 1 MLG1MANNACTKNWLAAPAA.....KSLTFSRWAEHLISFREK 334

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New.*

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6: /cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	1737	99.4	1005	US-10-272-983-35
2	1737	99.4	1436	US-10-264-237-1352
3	1720	98.5	1428	US-10-270-857-1
4	1720	98.5	1428	US-10-270-587-1
5	477	27.3	1014	US-10-270-144-1
6	477	27.3	1014	US-10-278-141-10
7	477	27.3	9905	US-10-270-144-3
8	384	22.0	2807	US-09-979-603A-1
9	384	22.0	2807	US-09-979-603-1
10	363.5	20.7	1922	US-10-152-319A-2068
11	348.5	19.9	1101	US-09-979-603A-17

12	348.5	19.9	1101	US-09-979-603-17	Sequence 17, Appl
13	343	19.6	1249	US-09-979-603A-21	Sequence 21, Appl
14	343	19.6	1249	US-09-979-603-21	Sequence 21, Appl
15	329	18.8	1451	US-09-958-805A-1	Sequence 1, Appl
16	323	18.5	3056	US-10-180-949-3	Sequence 3, Appl
17	321.5	18.4	2260	US-09-724-676-33307	Sequence 33307, A
18	321.5	18.4	2260	US-09-724-676A-33307	Sequence 33307, A
19	321.5	18.4	2279	US-09-724-676-33306	Sequence 33306, A
20	321.5	18.4	2279	US-09-724-676A-33306	Sequence 33306, A
21	321.5	18.4	2344	US-09-724-676A-33308	Sequence 33308, A
22	321.5	18.4	2344	US-09-724-676A-33308	Sequence 33308, A
23	317.5	18.2	2051	US-10-240-425-1201	Sequence 1201, Ap
24	316	18.1	1450	US-10-152-319A-1852	Sequence 1852, Ap
25	313	17.9	1014	US-10-152-319A-1561	Sequence 1561, Ap
26	311.5	17.8	1285	US-10-273-575-3	Sequence 3, Appl
27	311	17.8	1285	US-10-273-575-3	Sequence 2, Appl
28	311	17.8	1285	US-10-265-872-2	Sequence 2, Appl
29	311	17.8	2156	US-10-152-319A-1856	Sequence 1856, Ap
30	310.5	17.8	1428	US-10-152-319A-2045	Sequence 2045, Ap
31	310.5	17.8	1904	US-10-180-949-1	Sequence 1, Appl
32	306	17.5	1080	US-10-054-616A-12	Sequence 12, Appl
33	303	17.3	1134	US-10-180-933-1	Sequence 1, Appl
34	301.5	17.3	1689	US-10-283-028-1	Sequence 1, Appl
35	299.5	17.1	1193	US-10-283-028-3	Sequence 3, Appl
36	299	17.1	1788	US-10-270-333-134	Sequence 134, App
37	296.5	17.0	1116	US-10-283-028-5	Sequence 5, Appl
38	295.5	16.9	1053	US-10-282-837-9	Sequence 9, Appl
39	295.5	16.9	1113	US-10-282-837-9	Sequence 7, Appl
40	295.5	16.9	1113	US-10-282-837-7	Sequence 7, Appl
41	295.5	16.9	1147	US-09-721-495B-1	Sequence 1, Appl
42	292.5	16.7	1053	US-10-272-983-21	Sequence 21, Appl
43	292	16.7	1181	US-10-270-333-116	Sequence 116, App
44	289.5	16.6	990	US-10-270-333-116	Sequence 3, Appl
45	288.5	16.5	1147	US-09-721-495B-3	

ALIGNMENTS

RESULT 1
US-10-272-983-35
Sequence 35, Application US/10272983
GENERAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1

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: SEQ ID NO 35
: LENGTH: 1005
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-272-983-35

Alignment Scores:
Pred. No.: 6.6e-159 Length: 1005
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x US-10-272-983-35 (1-1005)

QY 1 MetLeuGlyIleMetValaTrpAsnAlaThrCysLysAsnTrpLeuAlaGluAla 20
DB 1 ATGCGTGGGATCATGGCATGGATGCAACTGGCAAAACTGGCTGGCAGAGGCTGCC 60
QY 21 LeuGluLysTrpTrpLeuSerIlePheTrpGlyIleGluPheValaGlyValLeuGly 40
DB 61 CTGGAAAGACTACCTTCATTTTATGGATGGATTGCTGTGGAGTCTTGGA 120
QY 41 AsnThrIleValIleValTrpGlyTrpIlePheSerLeuLysAsnTrpAsnSerAsnIle 60
DB 121 AATACCATGTTGTTTACGGCTACATCTTCTCTGAAAGAACTGGAAACAGATATATT 180
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 181 TATCTCTTAACTCTCTGCTGCTGACTTACCTTTCTGTGCACCCCTCCCATGCTGATA 240
QY 81 ArgSerTrpAlaAsnGlyAsnTrpIleTrpGlyAspValLeuCysIleSerAsnArgTyr 100
DB 241 AGGAGTATGCAATGGAATGCAATGATATATGAGACGCTGCTGATAGCAACCGATAT 300
QY 101 ValLeuHisAlaAsnLeuTrpThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 301 GTGCTTATGCAACCTCTATACAGCATCTCTCTTCTCCTCTTATATGATGATATGCA 360
QY 121 TyrLeuIleIleLysTrpProPheArgGluHisLeuLeuGlnLysGluPheAlaIle 140
DB 361 TACTGTGATTAATTAAGTATCCTTTCCGAGAACACCTCTGCAAAAGAAAGATTTGCTATT 420
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeu 160
DB 421 TTAATCTCTGGCCATTTGGGTTTACTTAACCTTAGAGTACTAACCATCTCTCCCTT 480
QY 161 IleAsnProValIleThrAspAsnGlyThrCysAsnAspPheAlaSerSerGlyAsp 180
DB 481 ATAAATCTCTTATATACGACATGACACGACCTGTAATGATTTTGGCAAGTTCTGGAGAC 540
QY 181 ProAsnTrpAsnLeuIleTrpSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
DB 541 CCCAACTACACCATTAATTAACGATGCTTAACACTGTTGGGGTTCCTTATTCCTCTT 600
QY 201 PheValMetCysPhePheTrpTrpLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
DB 601 TTTGTGAGTGTCTTCTTATTAACAGATTGCTCTCTCCCAAGCAAGAAAGAGGAG 660
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValAlaIle 240
DB 661 GTTCTACTGCTGCTGCCCCCTTGAAGAGCCTCTCAACTTGGTCATCATAGGCGTGTATTC 720
QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
DB 721 TTTCTCTGCGCTTTTACACCTATACAGTCACTGGGAATGAGAGATGCGTTCACGCGTGG 780
QY 261 GlySerTrpLysGlnTrpGlnCysThrGlnValValIleAsnSerPheTrpIleValThr 280
DB 781 GGGAGTTGGAAGAGATATCATGTCACATCAGGTCGTCATCAACTCTTTTACATGTTGACA 840
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTrpPheLeuLeuGlyAsp 300
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DB 841 CGGCTTTGGCTTCTGACAGTGTCAACACCTGCTCTTCTATTTCTTTGGAGAT 900
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
DB 901 CACTTCAGAGCAATGCTATGATATCACTGAGACCAACTCAATCCCTTACATCTTT 960
QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
DB 961 AGCAGATGGGCTCATGAACTCTCACTTCAATTCAGAGAAAG 1002

RESULT 2
US-10-264-237-1352
: Sequence 1352, Application US/10264237
: GENERAL INFORMATION:
: APPLICANT: Birs et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P131P1
: CURRENT APPLICATION NUMBER: US/10/264, 237
: CURRENT FILING DATE: 2002-10-04
: PRIOR APPLICATION NUMBER: PCT/US01/16450
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: US 60/205,515
: PRIOR FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 2876
: SOFTWARE: PatentIn Ver. 3.1
: SEQ ID NO 1352
: LENGTH: 1436
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-264-237-1352

Alignment Scores:
Pred. No.: 1.02e-158 Length: 1436
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x US-10-264-237-1352 (1-1436)

QY 1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaGluAla 20
DB 93 ATGCGTGGGATCATGGCATGGATGCAACTGGCAAAACTGGCTGGCAGAGGCTGCC 152
QY 21 LeuGluLysTrpTrpLeuSerIlePheTrpGlyIleGluPheValaGlyValLeuGly 40
DB 153 CTGGAAAGACTACCTTCATTTTATGATGAGTTCGCTTGGAGGAGTCTTGCA 212
QY 41 AsnThrIleValIleValTrpGlyTrpIlePheSerLeuLysAsnTrpAsnSerAsnIle 60
DB 213 AATACCATGTTGTTTACGGCTACATCTTCTCTGAAAGAACTGGAAACAGATATATT 272
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 273 TATCTCTTAACTCTCTGCTGACTTACCTTTCTGTGCACCCCTCCCATGCTGATA 332
QY 81 ArgSerTrpAlaAsnGlyAsnTrpIleTrpGlyAspValLeuCysIleSerAsnArgTyr 100
DB 333 AGGAGTATGCAATGGAATGATATATGAGACAGCTGCTGCTCATATACCAACCGATAT 392
QY 101 ValLeuHisAlaAsnLeuTrpThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 393 GTGCTTATGCAACCTTATACAGCATCTTCTTCTCACTTTTATACAGATGATGCA 452
QY 121 TyrLeuIleIleLysTrpProPheArgGluHisLeuLeuGlnLysGluPheAlaIle 140
DB 453 TACTGTATTAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGATTTGCTATT 512
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
DB 513 TTAATCTCTTGGCCATTTTGGGTTTATGATACCTTACAGTTACTAACCATTAATCTCCCTT 572
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QY	161	ILEASNPROVALIETRRASPANGLYTRTHCYASASPPhAlSesSerCLySP	180
Db	573	ATAAATCTGTTATACGTACAAATGGCACACCGCTGAATGATTTTGCAAGTTCGGAAAC	632
QY	181	PROASNTRYASNLEUIETYSerMetCYSLethrLeuLeuGlyPheLeuIleProLeu	200
Db	633	CCCAACACAACTCATTTACACAGATGTGTCAACAGCTTTGGGGTTCCTATTCCTCT	692
QY	201	PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgASNArgGln	220
Db	693	TTTGTGATGTGTTCTTTTATACAAAGATGTCTCTTCCTCAACAGACGAGATAGCAG	752
QY	221	ValAlaThrAlaLeuProLeuGlyLysProLeuASNLeuValIleMetAlaValAlaIle	240
Db	753	GTTCCTCTCTCTCTGGCCCCCTTGAAAGCCCTCAACTGGTGATATGGCACTGGTATTC	812
QY	241	PheSerValProPheThrProTyrHisValMetArgASNValArgIleAlaSerArgLeu	260
Db	813	TTCTCTGTGCTTTTATACACCCCTTATCACGTCATGCGGAATGTAGAGATGCTTCACGCTG	872
QY	261	GlySerTrpLysGlnTyrGlnCysThrGlnValIleASNSeSerPheTyrIleValThr	280
Db	873	GGGAGTGGGAAGCAGATACGTGCACTACAGTGTGTATCAATCCTTTTACATTTTGACA	932
QY	281	ArgProLeuAlaPheLeuASNSeValIleASNProValPheTyrPheLeuLeuGlyASP	300
Db	933	CGGCGCTTTGGCCCTTTTGAAACAGTGTGCATCAACACCCGTCTCTATTTCTTTGGGACAT	992
QY	301	HisPheArgASPheLeuMetASNLeuGlnLeuArgHisASNPhLysSerLeuThrSerPhe	320
Db	993	CACCTTCAGGGACATGCTGATGAATCAACAGACACAACTTCAAAATCCCTTACATCCTTT	1052
QY	321	SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGlyLys	334
Db	1053	AGCAGATGGGCTCATGAACTCCTACTTTCATTATTCAGGAAAG	1094

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RESULT 3
US-10-270-857-1
; Sequence 1, Application US/10270857
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; FILE REFERENCE: P217C2
; CURRENT APPLICATION NUMBER: US/10/270,857
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 09/908,593
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 08/781,456
; PRIOR FILING DATE: 1997-01-10
; PRIOR APPLICATION NUMBER: US 60/009,902
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-270-857-1

Alignment Scores:
Pred. No.:          4,42e-157          Length: 1428
Score:              1720.00             Matches: 329
Percent Similarity: 99.40%             Conservative: 3
Best Local Similarity: 98.50%           Mismatches: 2
Query Match:        98.45%             Indels: 0
DB:                  6                  Gaps: 0

US-09-765-034-2 (1-334) x US-10-270-857-1 (1-1428)

Oy      1 MetLeuGlyIleKekAlaIATPAsrAlaIrhCysLySAsnTrIpLeuAlaIaGluaIaIaIa 20
15b      92 ATGTGGGGAGCAACGATGGAAATGCAACTGTGCAAAAACGTGGCTGGCGACGAGGCTGCC 151

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QY	21	LeuGIuLySrYrTyrLeuSerIlePhePheYrGlyIleGluIlePheValAlaGlyValIleuGly	40
Db	152	CTGGAAAGAGTACACCTTTCACATTTTATATGGAGATTGAGTCTGTGGAGTCCCTTGGCA	211
QY	41	AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpPasnSerSerAsnIle	60
Db	212	AATACCATGTGTGTATACGGCTACATCTCTCTGTGAAGAACTGGAAACAGCATATATTT	271
QY	61	TyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCystrIleuProMetLeuIle	80
Db	272	TATCTCTTAACTCCTCTGCTCTGTGACTTAAAGCTTTTCTGTGACCCCTCCCATCTGATA	331
QY	81	ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValIleuCystrIleSerAsnArgTyr	100
Db	332	AGGAGTTATGCCAATGGAAAGCTGATATATGGAGACGTGCTGTGATATAGCAACCGATAT	391
QY	101	ValIleuHisAlaAsnLeuTyrThrSerIleLeuPheLeuTrpPheIleSerIleAspArg	120
Db	392	GTGCTCATGCCAACCCTATACAGCATCTCTTCTACCTTTATACGATATGATGCA	451
QY	121	TyrIleuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle	140
Db	452	TACTGTATATTAATTAAGATACCTTTCCGAGAACCTCTGCAAAAGAAAGATGGCTATT	511
QY	141	LeuIleSerIleuAlaIleTrpPheValIleValIleThrIleuGluIleuLeuProIleuProLeu	160
Db	512	TTAAATTCCTGGCCACATGGGGTTTATAGTAAACCTTAAAGGATACCAACCATCTCCCTT	571
QY	161	IleAsnProValIleThrAspAsnGlyThrTrpCysAsnAspPheAlaSerSerGlyAsp	180
Db	572	ATTAATCTCTTATTAAGTACGAAATGGCAACCACTGTATATGATTTTGCAGTTCTGGAGAC	631
QY	181	ProAsnTyrAsnLeuIleTyrSerMetCysIleuTrpLeuLeuGlyPheLeuIleProLeu	200
Db	632	CCCACTACACCACTCATTTACAGCATGTCTTAACACTGTGGGGTCCCTATCTCTCTT	691
QY	201	PheValMetCysPhePheTyrTyrLysIleAlaIleuPheLeuLysGlnIleAsnArgGln	220
Db	692	TTTCTGTATGGTTCCTTATTAACAAGATTGCTCTCTTCTTAAGACAGAGAAATAGGCAG	751
QY	221	ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValValIle	240
Db	752	GTTCCTACTGCTGTGCCCTTGAAAGCCTGTCAACTGTGTCAATCATATGCGCAGTGTATTC	811
QY	241	PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu	260
Db	812	TTCTCTGTGCTTTTACACCCCTATACGTCATCGCATGCGGAATGTAGAGATGGCTTACGCGCTG	871
QY	261	GlySerTrpLysGlnIleGlnCysTrpArgIleValIleAsnSerPheTyrIleValThr	280
Db	872	GGGAGTTTGAAGCAATACGTGACACTGACGTGCTCATCACTCTCTTAAATTTGTATACA	931
QY	281	ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp	300
Db	932	CGGCGCTGTGGCCTTTCGAACAGTGTCAATCAACCTGTCTTCATTTTCTTGTGGGAGAT	991
QY	301	HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerIleuTrpSerPhe	320
Db	992	CACCTTCAGGAGACATGCTGATGATCAATCAACAGAAACAACTCAATTCCTTACATCTTT	1051
QY	321	SerArgTrpAlaHisGluIleuLeuLeuSerPheArgGlyLys	334
Db	1052	AGCAGATGGCTCATGAACTCCACTTCTTATTTCAAGAAAG	1093

RESULT 4
US-10-270-587-1
Sequence 1, Application US/10270587
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Human G-Protein Coupled Receptor
FILE REFERENCE: P21A1C2
CURRENT APPLICATION NUMBER: US/10/2270,587


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Db 352 TATAGAGATCCTCTTCTCACTGTTACAGATCTTCCGCTACTGTGTGATCATTCAC 411
Oy 127 ProPheargGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db 412 CCAATGAGCTGCTTTTCATTCACAAACTCGATGTCGACGTGACCTGTGCTGGTG 471
Oy 147 TrpValLeuValThrLeuGlnLeuLeuPheProIleLeuProLeuIleAsnProValIleThr 166
Db 472 TGGATCATTTTCACCTGCTACTGTCATTCGATCCGATCCCTTGTTCACATCAACCAACAG 531
Oy 167 AspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAspProAsnTrpAsnLeuIle 186
Db 532 ACCACAGATCAGCTGCTGTCTCGACCTCACAGTTCGATGAGTCAATTAATTAAGTG 551
Oy 187 TyrSerMetCysLeuThrLeuLeuGlnPheLeuIleProLeuPheValMetCysPhePhe 206
Db 592 TACAACTGATTTTGCATCGCACTACTTCTGCTCCCTGGTGTGATGAGACACTTTCG 651
Oy 207 TyrTrpLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 652 TATACACACATTT---ATCCACACTCTGACCCACATGACAGCTCAACAGCTCCCTTAAG 708
Oy 227 LeuGluLysProLeuAsnLeuValIleMetAlaValIlePheSerValProPheThr 246
Db 709 ---CAGAAAGCAGAGAGCTAACCATTCCTGCTACTCTTCGATTTTACGTATGTTTTRA 765
Oy 247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
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Oy 267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValIleThrArgProLeuAlaPhe 285
Db 817 ACTGTGTCATTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 876
Oy 286 LeuAsnSerValIleLeuAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
Db 877 CGAAGACCTTTGCTGATCCTGTTACTATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 936
Oy 306 LeuMetAsnGlnLeuArg 311
Db 937 GTCCTCTCAACAGTGA 954

RESULT 6
US-10-278-141-10
; Sequence 10, Application US/10278141
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Alina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Fairah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALTA, Nairinder K.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 USA
; CURRENT APPLICATION NUMBER: US/10/278,141
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/208,834
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/207,566
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US01/16285
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; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205,628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208,861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/206,222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6575963CH1
US-10-278-141-10

Alignment Scores:
Pred. No.: 1,82e-37 Length: 1014
Score: 477.00 Matches: 110
Percent Similarity: 55.88 Conservative: 61
Best Local Similarity: 35.95 Mismatches: 123
Query Match: 27.308 Indels: 12
DB: Gaps: 6

US-09-765-034-2 (1-334) x US-10-278-141-10 (1-1014).
Oy 8 AsnAlaThrCysLysAsnTrpLeuAlaIleAlaLeuLysTrpTyrLeuSer 27
Db 67 AATTGCATGATGAAAC-----ATCCACTCAAGATGACATCTCCCT 111
Oy 28 IlePheTyrGlyIleGluPheValIleGlyValLeuGlyAsnThrIleValValTyrGly 47
Db 112 GTTATTATGAGCATATTCCTCCGCGGATTTCCAGGCAATGACATGATGATGACCT 171
Oy 48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
Db 172 TACATTTTCAAATGAGACCTTGGAAGACGACCATCATTTATGCTGAACCTGGCTCG 231
Oy 68 SerAspLeuAlaPheLeuLysThrLeuPheMetLeuIleArgSerTyrAlaAsnGly 86
Db 232 ACAGATCTGCTGATCTGACACAGCTCCCTTCTGATTCATCTACTATGCGACGTGCGAA 291
Oy 87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db 292 AACTGATCTTTGAGATTCATGCTGATGATTAATCCGCTTCAGCTTCATTCACCTG 351
Oy 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
Db 352 TATAGCAGATCCCTTCTCCTCACCTGTTCCAGCATCTCCGCTACGTGATCATTCAC 411
Oy 127 ProPheargGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db 412 CCAATGAGCTGCTTTTCATTCACAAACTCGATGTCAGTGTGCTGCTGCTGCTGCTGCTG 471
Oy 147 TrpValLeuValThrLeuGlnLeuLeuPheProIleLeuProLeuIleAsnProValIleThr 166
Db 472 TGGATCATTTTCACCTGCTACTGTCATTCGATCCGATCCCTTGTTCACATCAACCAACAG 531
Oy 167 AspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAspProAsnTrpAsnLeuIle 186
Db 532 ACCACAGATCAGCTGCTGTCTCGACCTCACAGTTCGATGAGTCAATTAATTAAGTG 551
Oy 187 TyrSerMetCysLeuThrLeuLeuGlnPheLeuIleProLeuPheValMetCysPhePhe 206
Db 592 TACAACTGATTTTGCATCGCACTACTTCTGCTCCCTGGTGTGATGAGACACTTTCG 651
Oy 207 TyrTrpLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 652 TATACACACATTT---ATCCACACTCTGACCCACATGACAGCTCAACAGCTCCCTTAAG 708
Oy 227 LeuGluLysProLeuAsnLeuValIleMetAlaValIlePheSerValProPheThr 246
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Db 709 ---CAGAAAGCAGAGGCTAACCACTTCTGCTACCTGCTGCTTGTATGTTTGA 765
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 247 ProTyrlHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 766 CCGTCGATATCTTGAGGCGATCGGATCGAGATCTCGCTGCTTCA-----ATC 816
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 AGCTGCTCCATTGAGAAATCAGATCCATGACCTTACATCGTTTCATGACCATTAAGCTCT 876
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 CTGAACACCTTGTGTAACCTGTTACTATATGTGTGTGTCAGAGCAACTTTCAGCAGGCT 936
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 306 LeuMetAsnGlnLeuArg 311
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 937 GTCGCTCAACAGTGAGA 954
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-10-270-144-3
: Sequence 3, Application US/10270144
: GENERAL INFORMATION:
: APPLICANT: WEI, Ming-Hui et al
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: CLO00750CON
: CURRENT APPLICATION NUMBER: US/10/270,144
: PRIOR FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/205,196
: PRIOR FILING DATE: 2000-05-18
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 9905
: TYPE: DNA
: ORGANISM: Human
US-10-270-144-3

Alignment Scores:
Pred. No.: 2,97e-36 Length: 9905
Score: 477.00 Matches: 110
Percent Similarity: 55.88% Conservative: 61
Best Local Similarity: 35.95% Mismatches: 123
Query Match: 27.30% Indels: 12
DB: Gaps: 6

US-09-765-034-2 (1-334) x US-10-270-144-3 (1-9905)
Qy 8 AsnAlaThrCysLysAsnTrpLeuAlaIleAlaIleAlaLeuGlyLysTyrTyrLeuSer 27
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8375 AATGCACTGATGGAAC-----ATCCCACTCAGATGACATCTACTCTCCCT 8419
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8420 GTTATTATGTCATATCTTCTCTGTCGGGATTTCCAGGCAATGCGATGATATCCACT 8479
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8480 TACATTTTCAAAATGAGACCTTGGAAGAGCAGACCATCATTAATGCTAAGCTGCCGCG 8539
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8540 ACAAGATCTGCTGATCTGACACCGCTCCCTCTGATTCACCTACTATGCGGAGCGGAA 8539
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8600 AACTGGATCTTGGAGATTCATGTAGTTTATCCGCTCACTCCATTCACACCTG 8659
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8660 TATATGACGACATCCCTTCCTGACCTGTTTCAGCATCTTCGCGCTACTGTGATCATTCAC 8719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 127 PropHeArgGlnHisLeuLeuGlnLysGluProIleAlaIleLeuIleSerLeuAlaIle 146
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8720 CCAATGAGCTGCTTTTCCATTCACAAACCTCGATGCGAGTTGTGCGCTGCTGGTG 8779
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 147 TrpValIleValThrLeuGlnLeuLeuProIleLeuProIleAsnProValIleThr 166
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8780 TGGATCATTTTCACTGCTGATGCTGTCTTCCTCGATGACCTTCTGATACATCAACACAGG 8839
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8840 ACCAACAGATGAGCTGCTGTCGACCTCAACAGTTGCGATGAACTGATATTAAGTG 8899
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8900 TACAACCTGATTTGCTGCAACTACTTTTCTCCCTCCCTGCTGATGATGTCACACTTGGC 8959
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgIleValAlaIleThrAlaLeuPro 226
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8960 TATACACAGATT---ATCCACACTGTGACCCATGAGCTGCAAACTGACAGCTGCTTAAG 9016
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 227 LeuGlnLysProLeuAsnLeuValIleMetAlaValIlePheSerValProPheThr 246
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9017 ---CAGAAAGCAGAGGCTAACCACTTCTGCTACTCTGATTTTGTATGTTTGA 9073
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 247 ProTyrlHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9074 CCGTCGATATCTTGAGGCGATGCTGATCGATCGAATCTCGCTGCTTCA-----ATC 9124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9125 AGCTGCTCATTTGAGAAATCAGATCCATGACCTTACATCGTTTCTAGACATTAAGCTCT 9184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9185 CTGAACACCTTGTGTAACCTGTTACTATATGTGTGTGTCAGAGCAAACTTTCAGCAGGCT 9244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 306 LeuMetAsnGlnLeuArg 311
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9245 GTCGCTCAACAGTGAGA 9262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-979-603A-1
: Sequence 1, Application US/09979603A
: GENERAL INFORMATION:
: APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.
: TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR
: FILE REFERENCE: 067335
: CURRENT APPLICATION NUMBER: US/09/979,603A
: PRIOR FILING DATE: 2001-11-16
: PRIOR APPLICATION NUMBER: PCT/JP00/06265
: PRIOR FILING DATE: 2000-09-13
: PRIOR APPLICATION NUMBER: JP 11-259986
: PRIOR FILING DATE: 1999-09-14
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 2807
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (264)..(1301)
: OTHER INFORMATION:
US-09-979-603A-1

Alignment Scores:
Pred. No.: 5.82e-28 Length: 2807
Score: 384.00 Matches: 102
Percent Similarity: 47.92% Conservative: 59
Best Local Similarity: 30.36% Mismatches: 125
Query Match: 21.98% Indels: 50
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DB: 5 Gaps: 11

US-09-765-034-2 (1-334) x US-09-979-603A-1 (1-2807)

OY 8 AsnAlaIleThrCysLysAsnTrpLeuAlaIleGluAlaIleLeuGluLysTyr----- 24

DB 321 AATGGCACCCTTACAGCAATTAACACAGGAGCACTGCACATTTGAAACTTCAAGACAGAA 380

OY 25 TyrLeuSerIlePheThyGlyIleGluPheValIleGlyValIleLeuGlyAsnThrIleVal 44

DB 381 TTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTGGGAAATGGTTGTC 440

OY 45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64

DB 441 ATATATGTTTCTCCAGCCTTATTAAGAGTCCACATCTGTACAGTTCATGCTTAAT 500

OY 65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuPrometLeuIleArgSerTyrAla 84

DB 501 CTGGCCATTCTCGATCTCTGTTCAATAGCAGCCTTCCCTTACGGCTGACATTAATCTT 560

OY 85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103

DB 561 AGAGCCTCAATGTGATATTTGAGACCTGGCCTGAGGATTAATGCTTAATCTGAT 620

OY 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrIleu 123

DB 621 GTCAACATGTACAGCAATTAATTTCTGACCGTGTAGTGTGCTGCTTCCGGCA 680

OY 124 IleLysTyrProPheArg---GluHisLeuLeuGluLysGluPheAlaIleLeu 142

DB 661 ATGGTTCACCCCTTTCGGCTTCTGCATGTCACACAGCATCAGAGCTCGATCTCTGT 740

OY 143 SerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleuProLeuIleAsn 162

DB 741 GGGATC---ATATGATCTCTTATCATGGCTTCTCAATATGCTCTG----- 785

OY 163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182

DB 786 -----GACAGTGGCTCTGTGAGCAAGCGCATGTGCATCA----- 821

OY 183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu----- 193

DB 822 -----TGCCTTAGAGCTGAATCTCTAATAAATTCCTTAAGCTGCAG 860

OY 194 -----LeuGlyPheLeuIleProLeuPheValMetCysPhe 205

DB 861 ACCATGACTATATGCTTGGTGGGCTGCTGCTGCTGCATTTTTCACACTCAGACATC 920

OY 206 PheTyrTyrLys---IleAlaLeuPheLeuLysGluAsnArgIleValAlaThrAla 224

DB 921 TGTATCTGCTGATCATTCGGTCTGTGTAAAGTGAGAGTCCAGAAATCGGGGCTGCGG 980

OY 225 LeuProLeuGluLysProLeuAsnLeuValIleMetAlaValIlePheSerValPro 244

DB 961 GTTTCACAGAGAGGACTGACACCATCATCATACCTTGATCATCTTCTTCTGTGT 1040

OY 245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuLysSerTyrLys 264

DB 1041 TTCCTGCCCTATCACACACTGAGGACCTC-----CACTTACGACATGGAAA 1088

OY 265 GlnTyrGlnCysThrGlnValIleAsnSerPheTyrIleValThrArgProLeuAla 284

DB 1089 GTGGGTTATGCAAAAGAC---AGACTGCAATAAGCTTGTGTTATCCACTGCGCTGGCA 1145

OY 285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304

DB 1146 GCAGCCAAATGCTGCTTCATCTCTGCTCTATTAATCTTGGGGAGAAATTTTAAGGAC 1205

OY 305 MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr 318

DB 1206 AGACTAAGGTCTGCACTGAGAAAAGGCAATCAGCAAGAGCAAAAGCA 1253

US-09-979-603-1

Sequence 1, Application US/09979603

GENERAL INFORMATION:

APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.

APPLICANT: Helix Research Institute

TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR

FILE REFERENCE: 067335

CURRENT APPLICATION NUMBER: US/09/979,603

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: PCT/JP00/06265

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: JP 11-259986

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 2807

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: exon

LOCATION: (264)..(1301)

OTHER INFORMATION:

US-09-979-603-1

Alignment Scores:

Pred. No.	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5,82e-28	2807	384.00	102	59	125	50	11
Percent Similarity:		47.92%					
Best Local Similarity:		30.36%					
Query Match:		21.98%					

US-09-765-034-2 (1-334) x US-09-979-603-1 (1-2807)

OY 8 AsnAlaIleThrCysLysAsnTrpLeuAlaIleGluAlaIleLeuGluLysTyr----- 24

DB 321 AATGGCACCCTTACAGCAATTAACACAGGAGCACTGCACATTTGAAACTTCAAGACAGAA 380

OY 25 TyrLeuSerIlePheThyGlyIleGluPheValIleGlyValIleLeuGlyAsnThrIleVal 44

DB 381 TTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTTGGGAAATGGTTGTC 440

OY 45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64

DB 441 ATATATGTTTCTCCAGCCTTATTAAGAGTCCACATCTGTACAGTTCATGCTTAAT 500

OY 65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuPrometLeuIleArgSerTyrAla 84

DB 501 CTGGCCATTCTCGATCTCTGTTCAATAGCAGCCTTCCCTTACGGCTGACATTAATCTT 560

OY 85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103

DB 561 AGAGCCTCAATGTGATATTTGAGACCTGGCCTGAGGATTAATGCTTAATCTGAT 620

OY 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrIleu 123

DB 621 GTCAACATGTACAGCAATTAATTTCTGACCGTGTAGTGTGCTGCTTCCGGCA 680

OY 124 IleLysTyrProPheArg---GluHisLeuLeuGluLysGluPheAlaIleLeu 142

DB 661 ATGGTTCACCCCTTTCGGCTTCTGCATGTCACACAGCATCAGAGCTCGATCTCTGT 740

OY 143 SerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleuProLeuIleAsn 162

DB 741 GGGATC---ATATGATCTCTTATCATGGCTTCTCAATATGCTCTG----- 785

OY 163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182

DB 786 -----GACAGTGGCTCTGAGCAAGGAGCATGTGCATCA----- 821

OY 183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu----- 193

